

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: <b>Papathanassiou et al.</b>	)	Examiner: <b>To be assigned</b>
Application No. <b>To be Assigned</b>	)	
Filed: <b>January 22, 2001</b>	)	Art. Unit: <b>To be assigned</b>
For: <b>Compositions and Methods</b>	)	
<b>For Inhibiting Cellular</b>	)	
<b>Proliferation</b>	)	

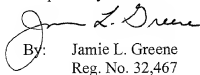
**TRANSMITTAL OF SEQUENCE LISTING UNDER 37 C.F.R. § 1.821(e)**

Assistant Commissioner of Patents  
Washington, D.C. 20231

Sir:

Applicants hereby submit a paper copy of the Sequence Listing for the application filed currently herewith. Pursuant to 37 C.F.R. § 1.821(e), a computer readable form is not included. The paper copy submitted herewith is identical to both the paper copy and the computer readable form that were previously submitted on January 11, 1999 in related U.S. Patent Application No. 09/227,955. Also pursuant to 37 C.F.R. § 1.821, no new matter, pertaining to the sequences as originally filed, has been added.

Respectfully submitted,

  
By: **Jamie L. Greene**  
Reg. No. 32,467

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Our Docket: 05213-0294 (KS # 43170-252538)



## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

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(i) APPLICANT: Papathanassiu, Adonia E  
Green, Shawn J.

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(ii) TITLE OF INVENTION: Compositions and Methods for  
Inhibiting Cellular Proliferation

(iii) NUMBER OF SEQUENCES: 2

15

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Jones & Askew
- (B) STREET: 191 Peachtree Street, 37th Floor
- (C) CITY: Atlanta
- (D) STATE: Georgia
- (E) COUNTRY: U.S.A.
- (F) ZIP: 30303

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(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

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(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US
- (B) FILING DATE:
- (C) CLASSIFICATION:

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(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Greene, Jamie L.
- (B) REGISTRATION NUMBER: 32,467
- (C) REFERENCE/DOCKET NUMBER: 05213-0290

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(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (404) 818-3700
- (B) TELEFAX: (404) 818-3799

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## (2) INFORMATION FOR SEQ ID NO:1:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 276 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens
- 20 (ix) FEATURE:  
 (A) NAME/KEY: Active-site  
 (B) LOCATION: 2..3  
 (D) OTHER INFORMATION: /note= "Site of partial  
 25 phosphorylation"
- (ix) FEATURE:  
 (A) NAME/KEY: Active-site  
 (B) LOCATION: 117..118  
 30 (D) OTHER INFORMATION: /note= "Potential site for N-linked  
 glycosylation"
- (ix) FEATURE:  
 (A) NAME/KEY: Active-site  
 35 (B) LOCATION: 167..168  
 (D) OTHER INFORMATION: /note= "Potential site for N-linked  
 glycosylation"
- (ix) FEATURE:  
 40 (A) NAME/KEY: Active-site  
 (B) LOCATION: 228..229  
 (D) OTHER INFORMATION: /note= "Potential site for N-linked  
 glycosylation"
- 45 (ix) FEATURE:  
 (A) NAME/KEY: Domain  
 (B) LOCATION: 26..76  
 (D) OTHER INFORMATION: /label= Kunitz-1



## (ix) FEATURE:

(A) NAME/KEY: Domain  
 (B) LOCATION: 97..147  
 (D) OTHER INFORMATION: /label= Kunitz-2

## (ix) FEATURE:

(A) NAME/KEY: Domain  
 (B) LOCATION: 189..239  
 (D) OTHER INFORMATION: /label= Kunitz-3

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

15 Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu  
 1 5 10 15

Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp  
 20 25 30

20 Gly Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr  
 35 40 45

25 Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn  
 50 55 60

Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn  
 65 70 75 80

30 Ala Asn Arg Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe  
 85 90 95

Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg  
 100 105 110

35 Tyr Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly  
 115 120 125

Gly Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys  
 130 135 140

40 Asn Ile Cys Glu Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly  
 145 150 155 160

45 Thr Gln Leu Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys  
 165 170 175

Val Pro Ser Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro  
 180 185 190



Ala Asp Arg Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn  
 195 200 205  
 5 Ser Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly  
 210 215 220  
 Asn Glu Asn Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys  
 225 230 235 240  
 10 Lys Gly Phe Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys  
 245 250 255  
 Arg Lys Arg Lys Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe  
 260 265 270  
 15 Val Lys Asn Met  
 275  
 20  
 25 (2) INFORMATION FOR SEQ ID NO:2:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 213 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 30  
 (ii) MOLECULE TYPE: protein  
 35 (iii) HYPOTHETICAL: NO  
 (iv) ANTI-SENSE: NO  
 40 (v) FRAGMENT TYPE: N-terminal  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens  
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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

5      Asp Ala Ala Gln Glu Pro Thr Gly Asn Asn Ala Glu Ile Cys Leu Leu  
       1                    5                    10                    15  
       Pro Leu Asp Tyr Gly Pro Cys Arg Ala Leu Leu Leu Arg Tyr Tyr Tyr  
                   20                    25                    30  
 10     Asp Arg Tyr Thr Gln Ser Cys Arg Gln Phe Leu Tyr Gly Gly Cys Glu  
                   35                    40                    45  
       Gly Asn Ala Asn Asn Phe Tyr Thr Trp Glu Ala Cys Asp Asp Ala Cys  
                   50                    55                    60  
 15     Trp Arg Ile Glu Lys Val Pro Lys Val Cys Arg Leu Gln Val Ser Val  
                   65                    70                    75                    80  
       Asp Asp Gln Cys Glu Gly Ser Thr Glu Lys Tyr Phe Phe Asn Leu Ser  
                   85                    90                    95  
 20     Ser Met Thr Cys Glu Lys Phe Phe Ser Gly Gly Cys His Arg Asn Arg  
                   100                    105                    110  
       Ile Glu Asn Arg Phe Pro Asp Glu Ala Thr Cys Met Gly Phe Cys Ala  
                   115                    120                    125  
       Pro Lys Lys Ile Pro Ser Phe Cys Tyr Ser Pro Lys Asp Glu Gly Leu  
                   130                    135                    140  
 30     Cys Ser Ala Asn Val Thr Arg Tyr Tyr Phe Asn Pro Arg Tyr Arg Thr  
                   145                    150                    155                    160  
       Cys Asp Ala Phe Thr Tyr Thr Gly Cys Gly Gly Asn Asp Asn Asn .Phe  
                   165                    170                    175  
       Val Ser Arg Glu Asp Cys Lys Arg Ala Cys Ala Lys Ala Leu Lys Lys  
                   180                    185                    190  
 40     Lys Lys Lys Met Pro Lys Leu Arg Phe Ala Ser Arg Ile Arg Lys Ile  
                   195                    200                    205  
       Arg Lys Lys Gln Phe  
                   210  
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